Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 13:05:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525009.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10525009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525009.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 13:05:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525009.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,440,028
Mapped reads	1,318,282 / 91.55%
Unmapped reads	121,746 / 8.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,781 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	37,233 / 2.59%
Duplication rate	1.99%
Clipped reads	1,319,634 / 91.64%

2.2. ACGT Content

Number/percentage of A's	18,456,370 / 24.31%
Number/percentage of C's	13,488,933 / 17.76%
Number/percentage of T's	25,044,196 / 32.98%
Number/percentage of G's	18,945,264 / 24.95%
Number/percentage of N's	694 / 0%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0245

Standard Deviation	0.2326

2.4. Mapping Quality

Mean Mapping Quality	44.04

2.5. Mismatches and indels

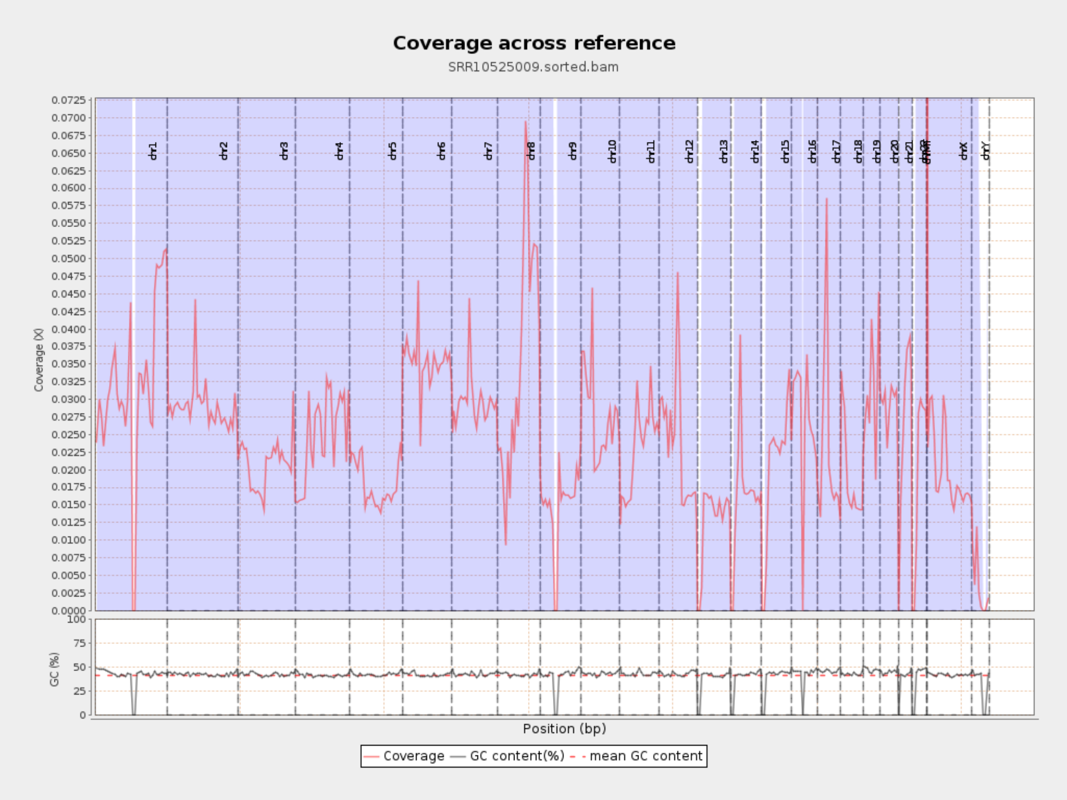
General error rate	0.51%
Mismatches	375,054
Insertions	5,023
Mapped reads with at least one insertion	0.38%
Deletions	14,268
Mapped reads with at least one deletion	1.08%
Homopolymer indels	43.49%

2.6. Chromosome stats

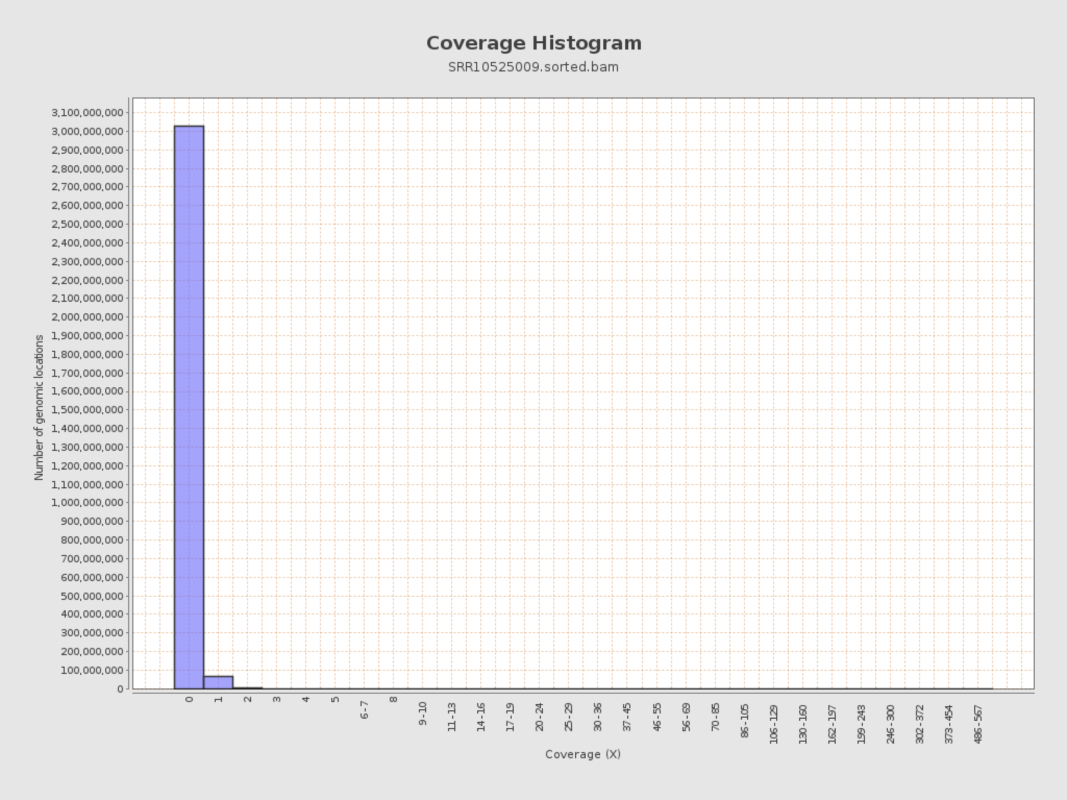
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7970781	0.032	0.4293
chr2	243199373	7051604	0.029	0.2781
chr3	198022430	4136143	0.0209	0.1554
chr4	191154276	4773435	0.025	0.1789
chr5	180915260	3263944	0.018	0.1454
chr6	171115067	6059424	0.0354	0.247
chr7	159138663	4737134	0.0298	0.3024

chr8	146364022	5276373	0.036	0.2366
chr9	141213431	2092711	0.0148	0.1718
chr10	135534747	3802463	0.0281	0.2293
chr11	135006516	3148980	0.0233	0.2118
chr12	133851895	3189893	0.0238	0.167
chr13	115169878	1457661	0.0127	0.1206
chr14	107349540	1733943	0.0162	0.1412
chr15	102531392	2095768	0.0204	0.1626
chr16	90354753	2412688	0.0267	0.1829
chr17	81195210	1908256	0.0235	0.2073
chr18	78077248	1482609	0.019	0.2707
chr19	59128983	1868178	0.0316	0.2827
chr20	63025520	1835032	0.0291	0.1836
chr21	48129895	1312816	0.0273	0.1827
chr22	51304566	1015707	0.0198	0.1494
chrMT	16571	8823	0.5324	0.7973
chrX	155270560	3119401	0.0201	0.173
chrY	59373566	205396	0.0035	0.0954

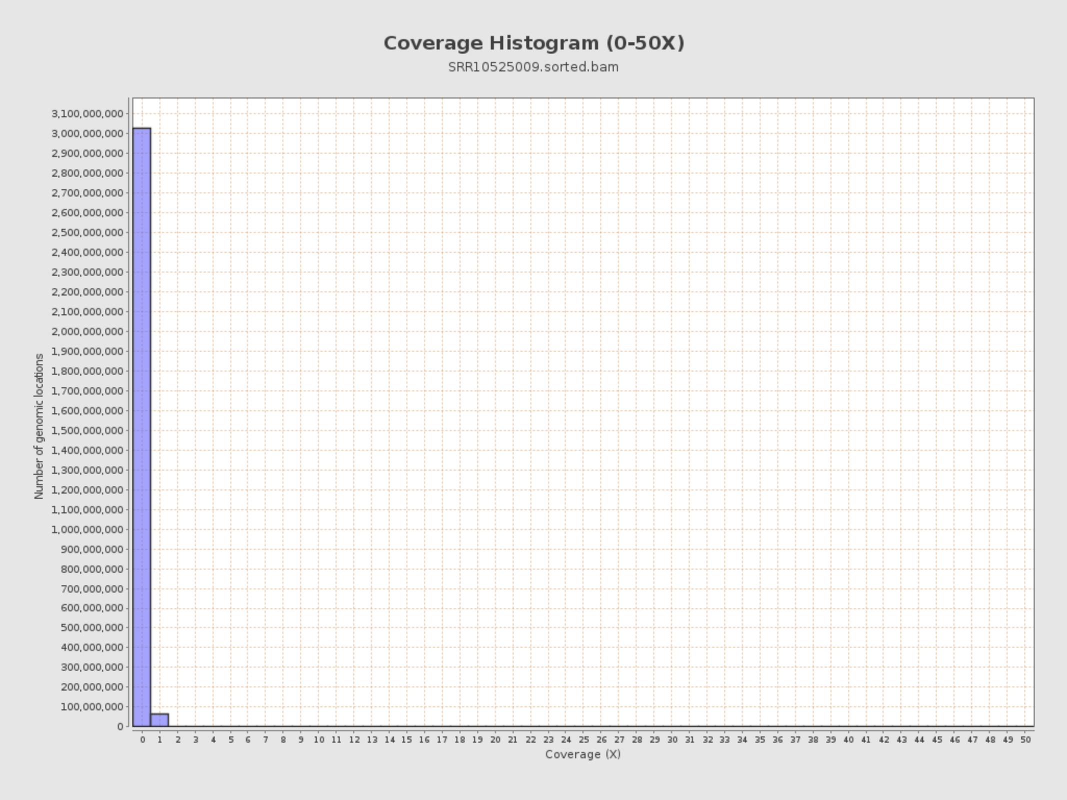
3. Results : Coverage across reference



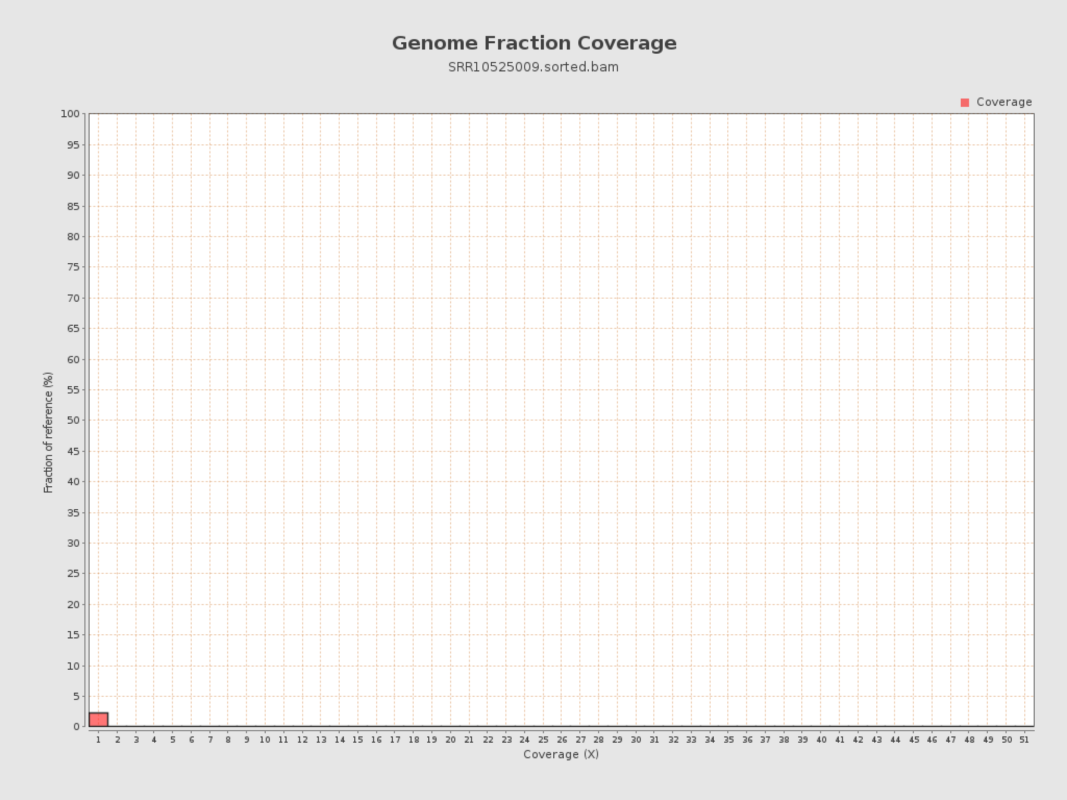
4. Results : Coverage Histogram



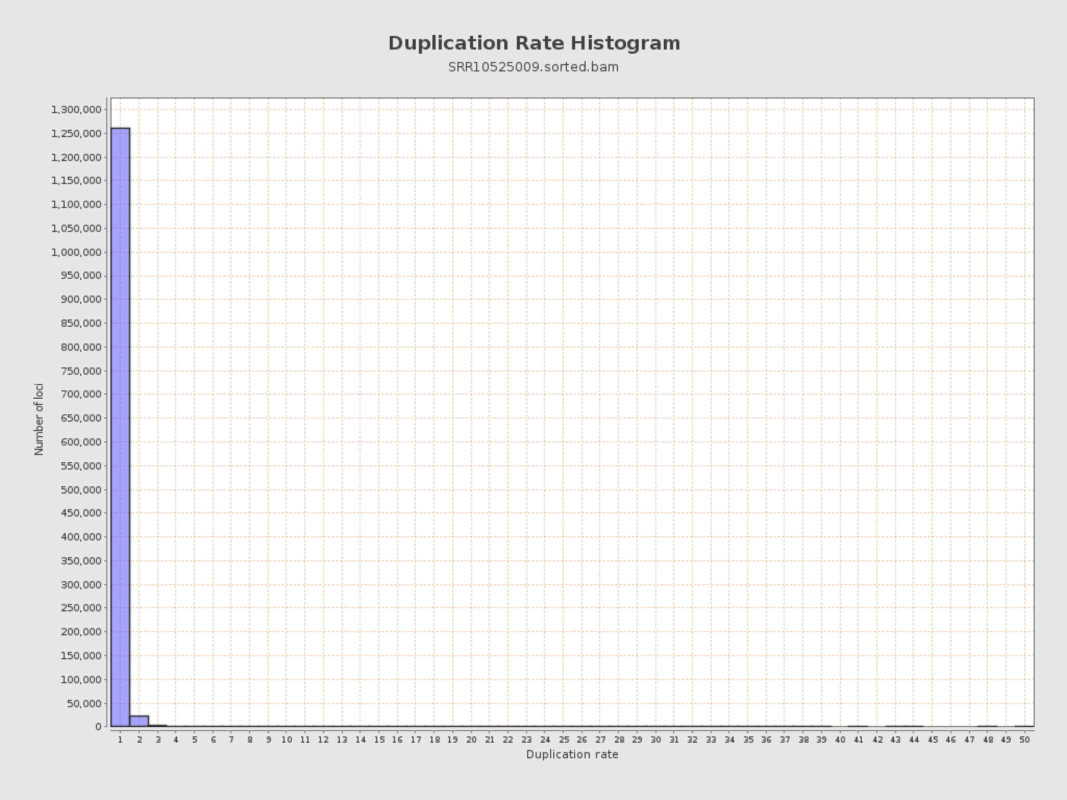
5. Results : Coverage Histogram (0-50X)



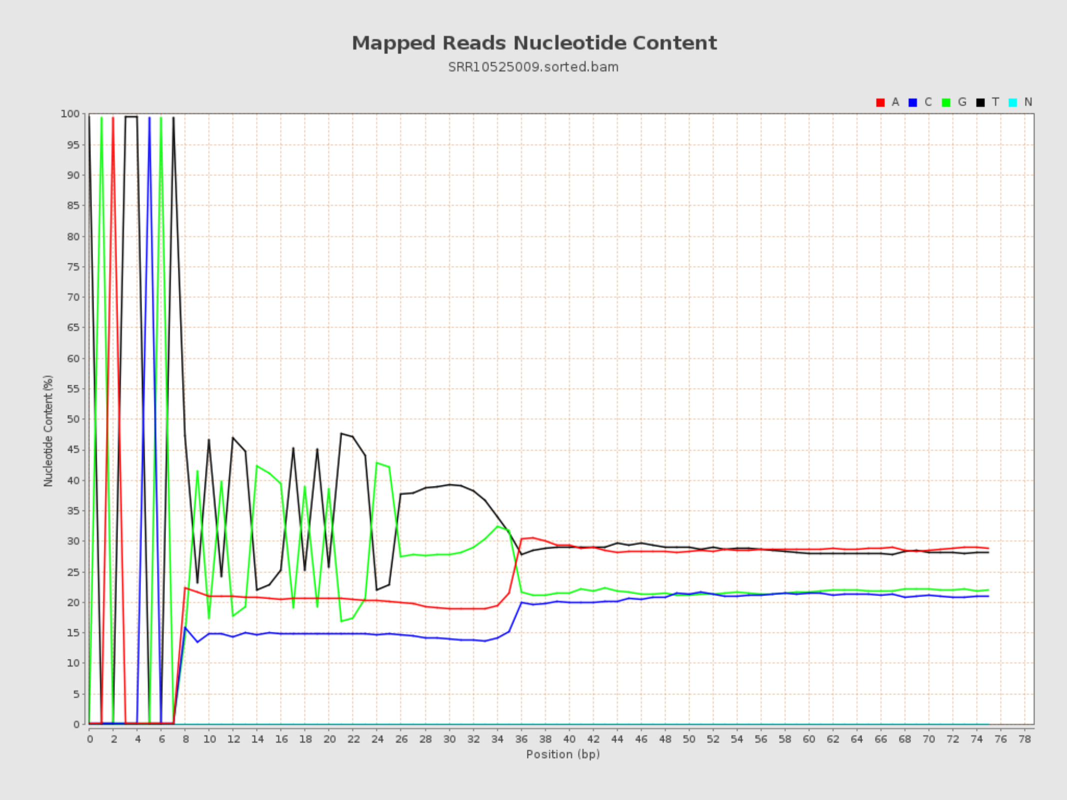
6. Results : Genome Fraction Coverage



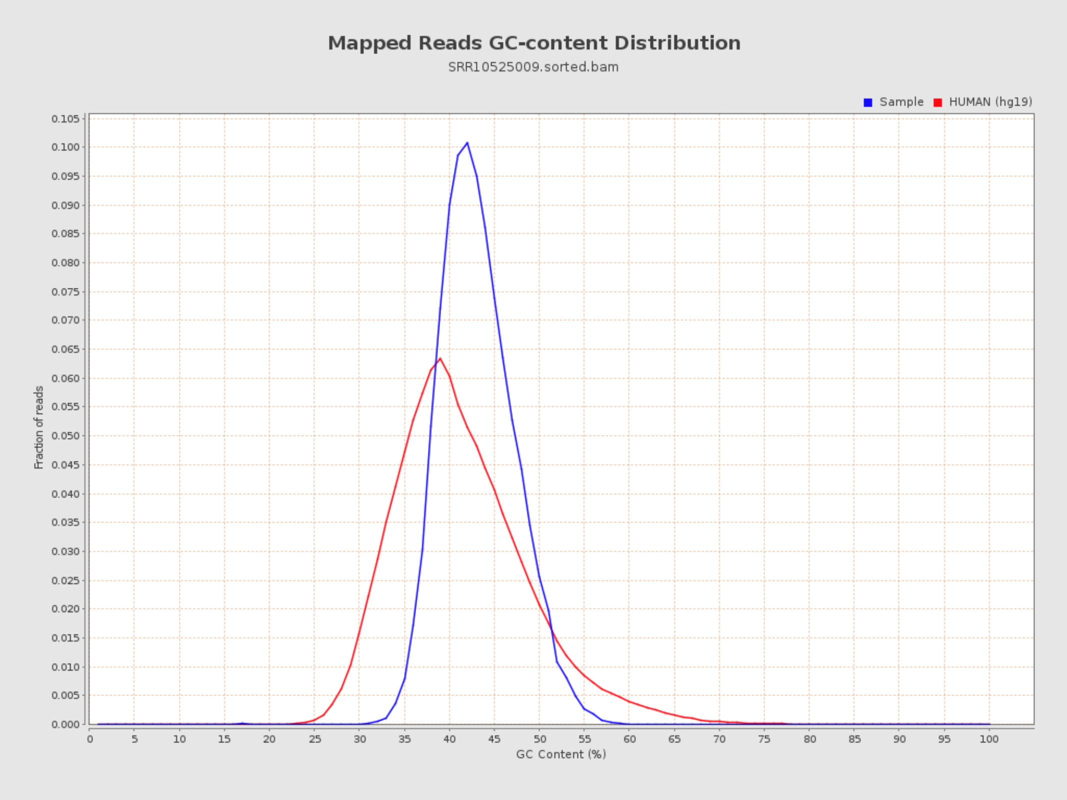
7. Results : Duplication Rate Histogram



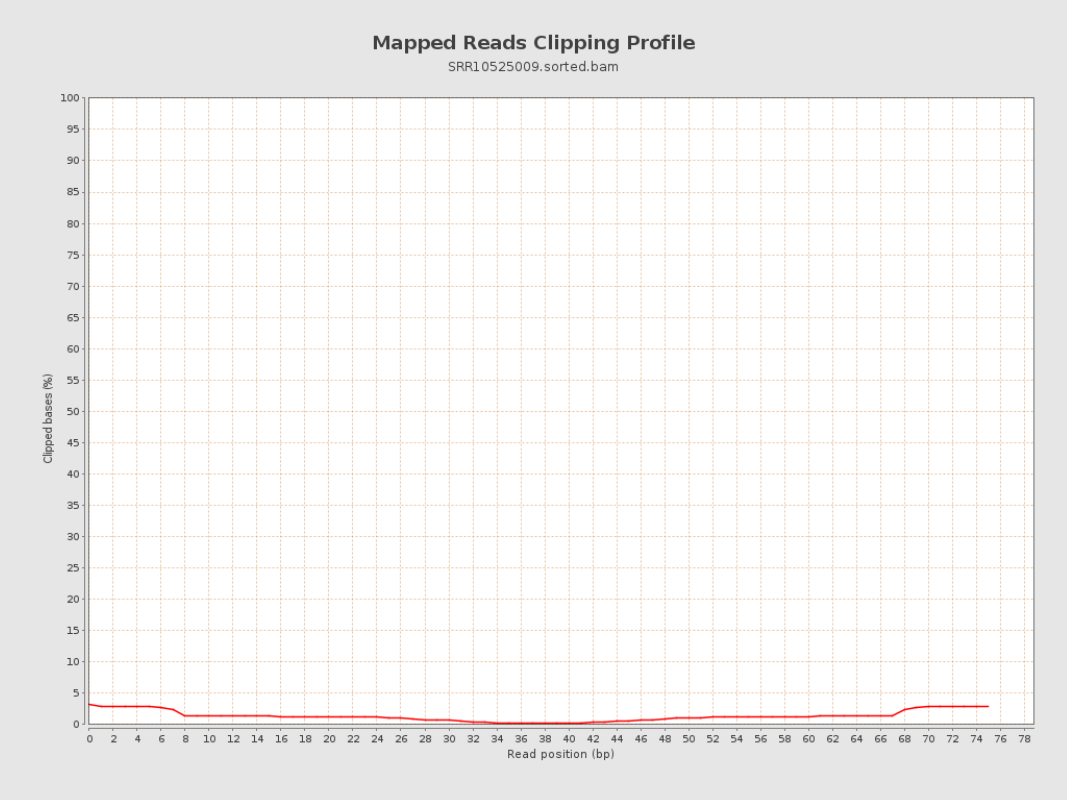
8. Results : Mapped Reads Nucleotide Content



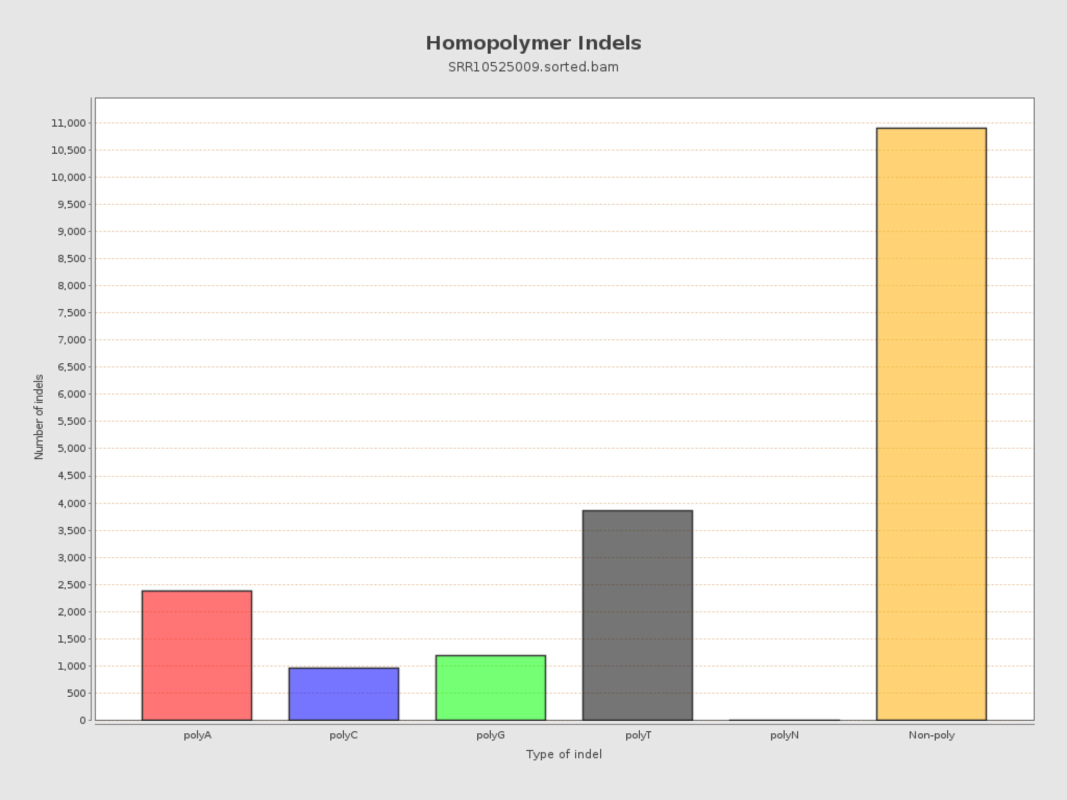
9. Results : Mapped Reads GC-content Distribution



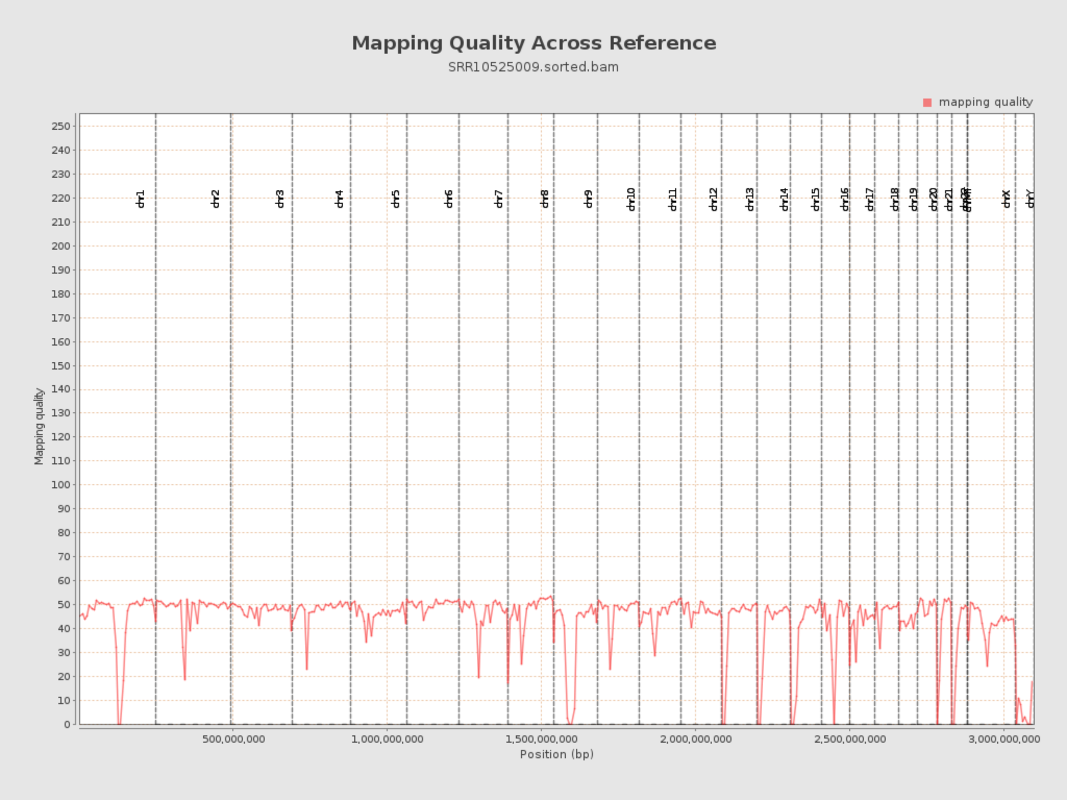
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram